

From: Chernyshev, Olga
Sent: Thursday, January 23, 2003 3:39 PM
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Please search US case 09/805,467 SEQ ID NO: 2.
Thank you very much!

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PAUL SCHULWITZ
TECHNICAL INFO. SPECIALIST
CM1 6B06 TEL. (703) 305-1954

Searcher: _____
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AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
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Other (specify): _____

EMBL:AC005849

ID AC005849 standard; DNA; HTG; 169144 BP.
XX
AC AC005849;
XX
SV AC005849.1
XX
DT 23-OCT-1998 (Rel. 57, Created)
DT 31-AUG-2001 (Rel. 68, Last updated, Version 4)
XX
DE Homo sapiens chromosome 11 clone CIT-HSP-1337H24, *** SEQUENCING IN
DE PROGRESS ***, 9 unordered pieces.
XX
KW HTG; HTGS_CANCELLED; HTGS_PHASE1.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-169144
RA Smith D.R.;
RT "Sequencing of Human Chromosome 10";
RL Unpublished.
XX
RN [2]
RP 1-169144
RA Smith D.R.;
RT ;
RL Submitted (22-OCT-1998) to the EMBL/GenBank/DDBJ databases.
RL Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02154,
USA
XX
DR SWISS-PROT; P57796; CAB4_HUMAN.
XX
CC * NOTE: This is a 'working draft' sequence. It currently
CC * consists of 9 contigs. The true order of the pieces
CC * is not known and their order in this sequence record is
CC * arbitrary. Gaps between the contigs are represented as
CC * runs of N, but the exact sizes of the gaps are unknown.
CC * This record will be updated with the finished sequence
CC * as soon as it is available and the accession number will
CC * be preserved.
CC * 1 506: contig of 506 bp in length
CC * gap of unknown length
CC * 507 3033: contig of 2527 bp in length
CC * gap of unknown length
CC * 3034 12956: contig of 9923 bp in length
CC * gap of unknown length
CC * 12957 19521: contig of 6565 bp in length
CC * gap of unknown length
CC * 19522 31636: contig of 12115 bp in length
CC * gap of unknown length
CC * 31637 48670: contig of 17034 bp in length
CC * gap of unknown length
CC * 48671 61610: contig of 12940 bp in length
CC * gap of unknown length
CC * 61611 97329: contig of 35719 bp in length
CC * gap of unknown length
CC * 97330 169144: contig of 71815 bp in length.
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FH Key Location/Qualifiers
FH

FT source 1..169144
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 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="CIT-HSP-1337H24"
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 SQ Sequence 169144 BP; 37524 A; 46225 C; 46279 G; 39089 T; 27 other;

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